

STIC-Biotech/ChemLib

87940

From: Schultz, James  
Sent: Monday, March 03, 2003 11:07 AM  
T : STIC-Biotech/ChemLib  
Subject: sequence search request for 10/003,919

Hello,

I need a length limited nucleotide sequence search performed on SEQ ID NO:3 (5273 nt long) in the above entitled case, where the maximum size of the returned hit is no longer than 50 nucleotides.  
Thank you very much,  
Doug Schultz

J. Douglas Schultz, Ph.D.  
AU 1635 (Biotechnology)  
Patent Examiner  
United States Patent and Trademark Office  
(703) 308-9355  
(703) 746-3973 (fax)  
Office: CM1 12E18  
Mail: CM1 11E12

Point of Contact:  
Barb O'Bryen  
Technical Information Specialist  
STIC CM1 6A05 308-4291

Searcher: 10013  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: 3-12-03  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

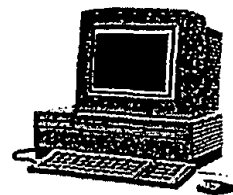
TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

# BioTech-Chem Library

## Search Results

### Feedback Form (Optional)



Scientific & Technical Information Center

The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact *the BioTech-Chem searcher* who conducted the search *or contact*:

Mary Hale, Supervisor, 308-4258  
CM-1 Room 1E01

---

#### *Voluntary Results Feedback Form*

- *I am an examiner in Workgroup:* (Example: 1610)
- *Relevant prior art found, search results used as follows:*
  - ☐ 102 rejection
  - ☐ 103 rejection
  - ☐ Cited as being of interest.
  - ☐ Helped examiner better understand the invention.
  - ☐ Helped examiner better understand the state of the art in their technology.

#### *Types of relevant prior art found:*

- ☐ Foreign Patent(s)
  - ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)
- *Relevant prior art not found:*
    - ☐ Results verified the lack of relevant prior art (helped determine patentability).
    - ☐ Search results were not useful in determining patentability or understanding the invention.

**Other Comments:**

---

Drop off completed forms at the Circulation Desk CM-1, or send to Mary Hale, CM1-1E01 or [mary.hale@uspto.gov](mailto:mary.hale@uspto.gov)

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using SW model

(Without alignments)  
11645.097 Million cell updates/sec

Sequence: 1 ctaggcattgcatcccaag.....aatgtgccttcttaaaa 5273

Scoring table: IDENTITY\_NUC

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Maximum DB seq length: 50

Post-processing: Minimum Match 08

Listing first 45 summaries

Database :

1: gb\_ba1: \*  
 2: gb\_h2: \*  
 3: gb\_in: \*  
 4: gb\_on: \*  
 5: gb\_ov: \*  
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 12: gb\_sy: \*  
 13: gb\_un: \*  
 14: gb\_v1: \*  
 15: em\_ba: \*  
 16: em\_fm: \*  
 17: em\_hum: \*  
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 37: em\_h2g\_vrt: \*  
 38: em\_h2g\_v1: \*  
 39: em\_h2g\_hum: \*  
 40: em\_h2g\_mu: \*  
 41: em\_h2g\_on: \*

Pred. No. is the number of results predicted by chance to have a

Result	Score	Query	Match	Length	DB	ID	Description
C 1	30.8	0.6	44	6	I31473	I31473	Sequence 38
C 2	30.6	0.6	31	6	BD002934	BD002934	Gene comp
C 3	30.6	0.6	31	6	BD002935	BD002935	Gene comp
C 4	30.6	0.6	31	6	BD002936	BD002936	Gene comp
C 5	30.6	0.6	31	6	BD002937	BD002937	Gene comp
C 6	30.6	0.6	31	6	BD002938	BD002938	Gene comp
C 7	30.6	0.6	31	6	BD002939	BD002939	Gene comp
C 8	30.6	0.6	31	6	BD002940	BD002940	Gene comp
C 9	30.6	0.6	31	6	BD002941	BD002941	Gene comp
C 10	30.6	0.6	31	6	BD002942	BD002942	Gene comp
C 11	30.6	0.6	31	6	BD002943	BD002943	Gene comp
C 12	28.4	0.5	50	6	AI178318	AI178318	Sequence
C 13	28.4	0.5	50	6	AI178319	AI178319	Sequence
C 14	25.8	0.5	50	6	AX323400	AX323400	Sequence
C 15	25.8	0.5	50	6	AX057285	AX057285	Sequence
C 16	24.8	0.5	43	8	YSCMP032	YSCMP032	Yeast (S. ce
C 17	24.8	0.5	30	6	AR208348	AR208348	Sequence
C 18	24.8	0.5	38	6	AX207477	AX207477	Sequence
C 19	24.8	0.5	43	8	YSCMP031	YSCMP031	Yeast (S. ce
C 20	24.4	0.5	27	6	AI175242	AI175242	Sequence
C 21	23.6	0.4	28	6	AR208346	AR208346	Sequence
C 22	23.6	0.4	32	6	AR002289	AR002289	Sequence
C 23	23.4	0.4	34	6	AR053140	AR053140	Sequence
C 24	23.4	0.4	34	6	AR001554	AR001554	Sequence
C 25	23.4	0.4	35	6	AR001553	AR001553	Sequence
C 26	23.4	0.4	36	6	AR001552	AR001552	Sequence
C 27	23.4	0.4	37	6	AR001551	AR001551	Sequence
C 28	23.4	0.4	38	6	AR001550	AR001550	Sequence
C 29	23.4	0.4	39	6	AR001549	AR001549	Sequence
C 30	23.4	0.4	40	6	AR001548	AR001548	Sequence
C 31	23.4	0.4	41	6	AR001547	AR001547	Sequence
C 32	23.4	0.4	42	6	AR001546	AR001546	Sequence
C 33	23.4	0.4	43	6	AR001545	AR001545	Sequence
C 34	23.4	0.4	45	6	AR001543	AR001543	Sequence
C 35	23.4	0.4	47	12	SYNPRMA	SYNPRMA	Artificial
C 36	23.2	0.4	50	6	AI158294	AI158294	Sequence
C 37	23.2	0.4	33	6	AI183778	AI183778	Sequence
C 38	23	0.4	43	6	AX484515	AX484515	Sequence
C 39	23	0.4	45	6	AR083212	AR083212	Sequence
C 40	22.8	0.4	47	6	AX378317	AX378317	Sequence
C 41	22.6	0.4	50	6	AI165890	AI165890	Sequence
C 42	22.4	0.4	48	6	AR064450	AR064450	Sequence
C 43	22.4	0.4	48	6	AR026545	AR026545	Sequence
C 44	22.4	0.4	24	6	AR026546	AR026546	Sequence
C 45	22.4	0.4	24	6	AR026547	AR026547	Sequence
C 46	22.4	0.4	24	6	AR026548	AR026548	Sequence

## ALIGNMENTS

RESULT 1	131473/c	44 bp	DNA	linear	PAT 06-FEB-1995
LOCUS	131473				
DEFINITION	Sequence 385 from patent US 5582979.				
ACCESSION	131473				
VERSION	131473.1				
KEYWORDS	GI:162264				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 44)				
TITLE	Weber, J.L.				
	Length polymorphisms in (dc-da).sub.n.(dg-dr).sub.n sequences and				

Patent: US 5582979-A 385 10-DEC-1996;

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Best Local Similarity	96.8%: Pred. No. 1.1e+05;		
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BD002936		31 bp	DNA linear PAT 31-JAN-2002
LOCUS			
DEFINITION	Gene composition and method.		
ACCESSION	BD002936		
VERSION	BD002936.1 GI:18630897		
KEYWORDS	JP 2000245487-A/602.		
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 31)		
AUTHORS	Sha, N., Walinton, J. and Patel, N.		
TITLE	Gene composition and method		
JOURNAL	Patent: JP 2000245487-A 602 12-SEP-2000;		
COMMENT	AFIMETRICS INC		
OS	Unknown		
PN	JP 2000245487-A/602		
PD	12-SEP-2000		
PP	27-JAN-2000 JP 2000019392		
PR	27-JAN-1999 US 09/238,402		
PI	NIRA SHA, JANET WALINTON, NIRA PATEL		
PC	C12N15/09, C12Q1/68, C12N15/00		
CC			
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Best Local Similarity	96.8%: Pred. No. 1.1e+05;		
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QY	1535 GAAATTCCTGCAGCTCATTAAGTCACAGAA 1565		
Db	1 GAAATTCCTGCAGCTCATTAAGTCACAGAA 31		
RESULT 5			
BD002937		31 bp	DNA linear PAT 31-JAN-2002
LOCUS			
DEFINITION	Gene composition and method.		
ACCESSION	BD002937		

VERSION BD002937.1 GI:18630898  
KEYWORDS JP 2000245487-A/603.  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Sha,N., Walinton,J. and Patel,N.  
TITLE Gene composition and method  
JOURNAL Patent: JP 2000245487-A 603 12-SEP-2000;  
AFIMETRICS INC  
COMMENT OS Unknown  
PN JP 2000245487-A/603  
PD 12-SEP-2000  
PR 27-JAN-2000 JP 2000019392  
PI NIRA SHA,JANET WALINTON,NIRA PATEL  
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OY 3464 TCCGAGACACAGAGTCAGGCCCACTGAC 3494  
DB 1 TCCGAGACACAGAGTCAGGCCCACTGAC 31  
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BD002938 31 bp DNA linear PAT 31-JAN-2002  
LOCUS BD002938 Gene composition and method.  
DEFINITION  
ACCESSION BD002938  
VERSION BD002938.1 GI:18630899  
KEYWORDS JP 2000245487-A/604.  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Sha,N., Walinton,J. and Patel,N.  
TITLE Gene composition and method  
JOURNAL Patent: JP 2000245487-A 604 12-SEP-2000;  
AFIMETRICS INC  
COMMENT OS Unknown  
PN JP 2000245487-A/604  
PD 12-SEP-2000  
PR 27-JAN-2000 JP 2000019392  
PI NIRA SHA,JANET WALINTON,NIRA PATEL  
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Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3999 AACACCGAGCTCCGCTATCAGCGCAAGCACC 4029  
DB 1 AACACCGAGCTCCGCTATCAGCGCAAGCACC 31  
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RESULT 7  
BD002939 31 bp DNA linear PAT 31-JAN-2002  
LOCUS BD002939 Gene composition and method.  
DEFINITION  
ACCESSION BD002939  
VERSION BD002939.1 GI:18630900  
KEYWORDS JP 2000245487-A/605.  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Sha,N., Walinton,J. and Patel,N.  
TITLE Gene composition and method  
JOURNAL Patent: JP 2000245487-A 605 12-SEP-2000;  
AFIMETRICS INC  
COMMENT OS Unknown  
PN JP 2000245487-A/605  
PD 12-SEP-2000  
PR 27-JAN-2000 JP 2000019392  
PI NIRA SHA,JANET WALINTON,NIRA PATEL  
PC C12N15/09,C12Q1/68,C12N15/00  
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Best Local Similarity 96.8%; Pred. No. 1.1e+05;  
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 4069 CCATGCACTGAGCCCTCAGTACCTGCCAC 4099  
DB 1 CCATGCACTGAGCCCTCAGTACCTGCCAC 31  
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RESULT 8  
BD002940 31 bp DNA linear PAT 31-JAN-2002  
LOCUS BD002940 Gene composition and method.  
DEFINITION  
ACCESSION BD002940  
VERSION BD002940.1 GI:18630901  
KEYWORDS JP 2000245487-A/606.  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Sha,N., Walinton,J. and Patel,N.  
TITLE Gene composition and method  
JOURNAL Patent: JP 2000245487-A 606 12-SEP-2000;  
AFIMETRICS INC  
COMMENT OS Unknown  
PN JP 2000245487-A/606  
PD 12-SEP-2000  
PR 27-JAN-2000 JP 2000019392  
PI NIRA SHA,JANET WALINTON,NIRA PATEL  
PC C12N15/09,C12Q1/68,C12N15/00  
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FEATURES FT /organism='Unknown'.  
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Best Local Similarity 96.8%; Pred. No. 1.1e+05;  
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 4310 TCTGGGTCCCACTGCTCTGTGACTTGG 4340  
DB 1 TCTGGGTCCCACTGCTCTGTGACTTGG 31  
RESULT 9  
BD002941 31 bp DNA linear PAT 31-JAN-2002  
LOCUS BD002941  
DEFINITION Gene composition and method.  
ACCESSION BD002941  
VERSION BD002941.1 GI:18630902  
KEYWORDS JP 2000245487-A/607.  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Sha, N., Walinton, J. and Patel, N.  
TITLE Gene composition and method  
JOURNAL Patent: JP 2000245487-A 607 12-SEP-2000;  
AFIMETRIS INC  
COMMENT OS Unknown  
PN JP 2000245487-A/607  
PD 12-SEP-2000  
PF 27-JAN-2000 JP 2000019392  
PR 27-JAN-1999 US 09/238.402  
PI NIRA SHA,JANET WALINTON,NIRA PATEL  
PC C12N15/09,C12Q1/68,C12N15/00  
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Best Local Similarity 96.8%; Pred. No. 1.1e+05;  
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 GGGACCCCACTGCTCTGTGAGGCGCCATT 31  
RESULT 10  
BD002942 31 bp DNA linear PAT 31-JAN-2002  
LOCUS BD002942  
DEFINITION Gene composition and method.  
ACCESSION BD002942  
VERSION BD002942.1 GI:18630903  
KEYWORDS JP 2000245487-A/608.  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Sha, N., Walinton, J. and Patel, N.  
TITLE Gene composition and method  
JOURNAL Patent: JP 2000245487-A 608 12-SEP-2000;

COMMENT AFIMETRIS INC  
OS Unknown  
PN JP 2000245487-A/608  
PD 12-SEP-2000  
PF 27-JAN-2000 JP 2000019392  
PR 27-JAN-1999 US 09/238.402  
PI NIRA SHA,JANET WALINTON,NIRA PATEL  
PC C12N15/09,C12Q1/68,C12N15/00  
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Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 4722 GCTTAGCTAAGTCCCGCGGTTCGCGCAT 4752  
DB 1 GCTTAGCTAAGTCCCGCGGTTCGCGCAT 31  
RESULT 12  
AR178318/c 50 bp DNA linear PAT 20-APR-2002  
LOCUS AR178318  
COMMENT AFIMETRIS INC  
OS Unknown  
PN JP 2000245487-A/609  
PD 12-SEP-2000  
PF 27-JAN-2000 JP 2000019392  
PR 27-JAN-1999 US 09/238.402  
PI NIRA SHA,JANET WALINTON,NIRA PATEL  
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Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 GATCGACACATCATGATGTCACAAAGTGTGT 31  
RESULT 11  
BD002943 31 bp DNA linear PAT 31-JAN-2002  
LOCUS BD002943  
DEFINITION Gene composition and method.  
ACCESSION BD002943  
VERSION BD002943.1 GI:18630904  
KEYWORDS JP 2000245487-A/609.  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Sha, N., Walinton, J. and Patel, N.  
TITLE Gene composition and method  
JOURNAL Patent: JP 2000245487-A 609 12-SEP-2000;  
AFIMETRIS INC  
COMMENT OS Unknown  
PN JP 2000245487-A/609  
PD 12-SEP-2000  
PF 27-JAN-2000 JP 2000019392  
PR 27-JAN-1999 US 09/238.402  
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CC AAA78631 to AAA79262 represent sequence tags of human genomic DNA  
CC fragments containing polymorphic sites. The base occupying the  
CC polymorphic site is indicated using IUPAC-IUB nomenclature.  
XX  
SQ Sequence 31 BP; 5 A; 10 C; 8 G; 7 T; 1 other;

Query Match 0.6%; Score 30.6; DB 21; Length 31;  
Best Local Similarity 96.8%; Pred. No. 9.1e+02;  
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 983 GAGCCTCTCCGAGACATTTCTCAGCAGCTG 1013  
DB 1 GAGCCTCTCCGAGACATTTCTCAGCAGCTG 31

RESULT 4  
ID AAA79231 standard; DNA; 31 BP.

AC AAA79231;

DT 20-NOV-2000 (first entry)

DE Human genomic DNA polymorphic site sequence tag SEQ ID NO:601.

XX Human; genomic DNA; polymorphism; genome; allele-specific; primer;  
KW probe; hybridisation; polymorphic site; forensic; paternity testing;  
KM medicine; phenotypic trait; genetic analysis; genetic mapping; ds.

OS Homo sapiens.

PN BP1024200-A2.

PD 02-AUG-2000.

PF 26-JAN-2000; 2000EP-0250023.

PR 27-JAN-1999; 99US-0238402.

PA (AFY-) AFFYMETRIX INC.

PI Patil N, Shah N, Warrington JA;

DR WPI; 2000-500198/45.

XX Human genomic polymorphic nucleic acid segments, allele specific  
PT primers and probes, and methods of analysis, useful for e.g. forensics,  
PI paternity testing, genetic mapping,  
PS Claim 1; Page 22; 141pp; English.

CC The present invention describes a nucleic acid segment of 10-100  
CC contiguous bases chosen from one of 632 fragments (AAA78631 to  
CC AAA79262), where the segment comprises a polymorphic site or an  
CC immediately adjacent base, or the complement of the segment. Also  
CC described are: (1) an allele-specific oligonucleotide that hybridises to  
CC a segment of the novelty; (2) an isolated nucleic acid comprising a  
CC sequence of the novelty where the polymorphic site within the sequence is  
CC occupied by a base other than the reference base indicated in the  
CC specification; and (3) analysing a nucleic acid, comprising obtaining a  
CC nucleic acid from an individual, and determining a base occupying any one  
CC of the polymorphic sites of the novelty. The nucleic acid segments and  
CC method can be used to analyse an individual's nucleic acid sequences for  
CC the presence of polymorphisms. The method can also be used to test for a  
CC disease phenotype and correlate the presence of the phenotype with a  
CC particular polymorphism. The presence of polymorphic sites are useful  
CC for, e.g. forensics, paternity testing, correlation of polymorphisms  
CC with phenotypic traits and for genetic mapping of phenotypic traits.  
CC AAA78631 to AAA79262 represent sequence tags of human genomic DNA  
CC fragments containing polymorphic sites. The base occupying the  
CC polymorphic site is indicated using IUPAC-IUB nomenclature.

SQ Sequence 31 BP; 9 A; 7 C; 7 G; 7 T; 1 other;

Query Match 0.6%; Score 30.6; DB 21; Length 31;  
Best Local Similarity 96.8%; Pred. No. 9.1e+02;  
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1313 GACACGCTGTGTCATTCATGAGACAG 1343  
DB 1 GACACGCTGTGTCATTCATGAGACAG 31

RESULT 5  
ID AAA79232 standard; DNA; 31 BP.

AC AAA79232;

DT 20-NOV-2000 (first entry)

DE Human genomic DNA polymorphic site sequence tag SEQ ID NO:602.

XX Human; genomic DNA; polymorphism; genome; allele-specific; primer;  
KW probe; hybridisation; polymorphic site; forensic; paternity testing;  
KM medicine; phenotypic trait; genetic analysis; genetic mapping; ds.

OS Homo sapiens.

PN BP1024200-A2.

PD 02-AUG-2000.

PF 26-JAN-2000; 2000EP-0250023.

PR 27-JAN-1999; 99US-0238402.

PA (AFY-) AFFYMETRIX INC.

PI Patil N, Shah N, Warrington JA;

DR WPI; 2000-500198/45.

XX Human genomic polymorphic nucleic acid segments, allele specific  
PT primers and probes, and methods of analysis, useful for e.g. forensics,  
PI paternity testing, genetic mapping,  
PS Claim 1; Page 22; 141pp; English.

CC The present invention describes a nucleic acid segment of 10-100  
CC contiguous bases chosen from one of 632 fragments (AAA78631 to  
CC AAA79262), where the segment comprises a polymorphic site or an  
CC immediately adjacent base, or the complement of the segment. Also  
CC described are: (1) an allele-specific oligonucleotide that hybridises to  
CC a segment of the novelty; (2) an isolated nucleic acid comprising a  
CC sequence of the novelty where the polymorphic site within the sequence is  
CC occupied by a base other than the reference base indicated in the  
CC specification; and (3) analysing a nucleic acid, comprising obtaining a  
CC nucleic acid from an individual, and determining a base occupying any one  
CC of the polymorphic sites of the novelty. The nucleic acid segments and  
CC method can be used to analyse an individual's nucleic acid sequences for  
CC the presence of polymorphisms. The method can also be used to test for a  
CC disease phenotype and correlate the presence of the phenotype with a  
CC particular polymorphism. The presence of polymorphic sites are useful  
CC for, e.g. forensics, paternity testing, correlation of polymorphisms  
CC with phenotypic traits and for genetic mapping of phenotypic traits.  
CC AAA78631 to AAA79262 represent sequence tags of human genomic DNA  
CC fragments containing polymorphic sites. The base occupying the  
CC polymorphic site is indicated using IUPAC-IUB nomenclature.

SQ Sequence 31 BP; 13 A; 6 C; 5 G; 6 T; 1 other;

Query Match 0.6%; Score 30.6; DB 21; Length 31;  
Best Local Similarity 96.8%; Pred. No. 9.1e+02;  
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



XX 20-NOV-2000 (first entry)  
XX Human genomic DNA polymorphic site sequence tag SEQ ID NO:605.  
XX  
XX Human: genomic DNA; polymorphism; genome; allele-specific; primer;  
KM probe; hybridisation; polymorphic site; forensic; paternity testing;  
KM medicine; phenotypic trait; genetic analysis; genetic mapping; ds.  
XX  
OS Homo sapiens.  
XX  
PN EP1024200-A2.  
XX  
PD 02-AUG-2000.  
XX  
PF 26-JAN-2000; 2000EP-0250023.  
XX  
PR 27-JAN-1999; 99US-0238402.  
XX  
PA (AFFY-) AFFYMERIX INC.  
XX  
PI Patil N, Shah N, Warrington JA;  
XX  
DR WPI; 2000-500198/45.  
XX  
PT Human genomic polymorphic nucleic acid segments, allele specific  
PT primers and probes, and methods of analysis, useful for e.g. forensics,  
PT paternity testing, genetic mapping,  
XX  
PS Claim 1; Page 22; 141pp; English.  
XX  
CC The present invention describes a nucleic acid segment of 10-100  
CC contiguous bases chosen from one of 632 fragments (AA78631 to  
CC AA79262), where the segment comprises a polymorphic site or an  
CC immediately adjacent base, or the complement of the segment. Also  
CC described are: (1) an allele-specific oligonucleotide that hybridises to  
CC a segment of the novelty; (2) an isolated nucleic acid comprising a  
CC sequence of the novelty where the polymorphic site within the sequence is  
CC occupied by a base other than the reference base indicated in the  
CC specification; and (3) analysing a nucleic acid, comprising obtaining a  
CC nucleic acid from an individual, and determining a base occupying any one  
CC of the polymorphic sites of the novelty. The nucleic acid segments and  
CC method can be used to analyse an individual's nucleic acid sequences for  
CC the presence of polymorphisms. The method can also be used to test for a  
CC disease phenotype and correlate the presence of the phenotype with a  
CC particular polymorphism. The presence of polymorphic sites are useful  
CC for, e.g. forensics, paternity testing, correlation of polymorphisms  
CC with phenotypic traits and for genetic mapping of phenotypic traits.  
CC AA78631 to AA79262 represent sequence tags of human genomic DNA  
CC fragments containing polymorphic sites. The base occupying the  
CC polymorphic site is indicated using IUPAC-IUB nomenclature.  
XX  
SQ Sequence 31 BP; 7 A; 10 C; 8 G; 5 T; 1 other:  
Query Match 0.6%; Score 30.6; DB 21; Length 31;  
Best Local Similarity 96.8%; Pred. No. 9.1e+02;  
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 4069 CCATGCAGTGAAGCCCTCACTGAGCTGCCAC 4099  
DB 1 CCATGCAGTGAAGCCCTCACTGAGCTGCCAC 31  
RESULT 9  
ID AAA79236 standard; DNA: 31 BP.  
AC AAA79236;  
XX  
XX 20-NOV-2000 (first entry)  
XX Human genomic DNA polymorphic site sequence tag SEQ ID NO:606.  
XX

KM Human: genomic DNA; polymorphism; genome; allele-specific; primer;  
KM probe; hybridisation; polymorphic site; forensic; paternity testing;  
KM medicine; phenotypic trait; genetic analysis; genetic mapping; ds.  
XX  
OS Homo sapiens.  
XX  
PN EP1024200-A2.  
XX  
PD 02-AUG-2000.  
XX  
PF 26-JAN-2000; 2000EP-0250023.  
XX  
PR 27-JAN-1999; 99US-0238402.  
XX  
PA (AFFY-) AFFYMERIX INC.  
XX  
PI Patil N, Shah N, Warrington JA;  
XX  
DR WPI; 2000-500198/45.  
XX  
PT Human genomic polymorphic nucleic acid segments, allele specific  
PT primers and probes, and methods of analysis, useful for e.g. forensics,  
PT paternity testing, genetic mapping,  
XX  
PS Claim 1; Page 22; 141pp; English.  
XX  
CC The present invention describes a nucleic acid segment of 10-100  
CC contiguous bases chosen from one of 632 fragments (AA78631 to  
CC AA79262), where the segment comprises a polymorphic site or an  
CC immediately adjacent base, or the complement of the segment. Also  
CC described are: (1) an allele-specific oligonucleotide that hybridises to  
CC a segment of the novelty; (2) an isolated nucleic acid comprising a  
CC sequence of the novelty where the polymorphic site within the sequence is  
CC occupied by a base other than the reference base indicated in the  
CC specification; and (3) analysing a nucleic acid, comprising obtaining a  
CC nucleic acid from an individual, and determining a base occupying any one  
CC of the polymorphic sites of the novelty. The nucleic acid segments and  
CC method can be used to analyse an individual's nucleic acid sequences for  
CC the presence of polymorphisms. The method can also be used to test for a  
CC disease phenotype and correlate the presence of the phenotype with a  
CC particular polymorphism. The presence of polymorphic sites are useful  
CC for, e.g. forensics, paternity testing, correlation of polymorphisms  
CC with phenotypic traits and for genetic mapping of phenotypic traits.  
CC AA78631 to AA79262 represent sequence tags of human genomic DNA  
CC fragments containing polymorphic sites. The base occupying the  
CC polymorphic site is indicated using IUPAC-IUB nomenclature.  
XX  
SQ Sequence 31 BP; 2 A; 9 C; 9 G; 10 T; 1 other:  
Query Match 0.6%; Score 30.6; DB 21; Length 31;  
Best Local Similarity 96.8%; Pred. No. 9.1e+02;  
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 4310 TCTGGTCCCGACGCTCGCTTGTGTAATTGG 4340  
DB 1 TCTGGTCCCGACGCTCGCTTGTGTAATTGG 31  
RESULT 10  
ID AAA79237 standard; DNA: 31 BP.  
AC AAA79237;  
XX  
XX 20-NOV-2000 (first entry)  
XX Human genomic DNA polymorphic site sequence tag SEQ ID NO:607.  
XX  
XX Human: genomic DNA; polymorphism; genome; allele-specific; primer;  
KM probe; hybridisation; polymorphic site; forensic; paternity testing;  
KM medicine; phenotypic trait; genetic analysis; genetic mapping; ds.  
XX  
OS Homo sapiens.

XX EPI024200-A2.  
 XX 02-AUG-2000.  
 XX 26-JAN-2000; 2000EP-0250023.  
 XX 27-JAN-1999; 99US-0238402.  
 XX (AFFY-) AFFYMETRIX INC.  
 XX Patil N, Shah N, Warrington JA;  
 XX WPI; 2000-500198/45.  
 XX  
 XX Human genomic polymorphic nucleic acid segments, allele specific  
 PT primers and probes, and methods of analysis, useful for e.g. forensics,  
 PT paternity testing, genetic mapping,  
 XX  
 PS Claim 1; Page 22; 141pp; English.  
 CC The present invention describes a nucleic acid segment of 10-100  
 CC contiguous bases chosen from one of 632 fragments (AAA/8631 to  
 CC AAA/9262), where the segment comprises a polymorphic site or an  
 CC immediately adjacent base, or the complement of the segment. Also  
 CC described are: (1) an allele-specific oligonucleotide that hybridises to  
 CC a segment of the novelty; (2) an isolated nucleic acid comprising a  
 CC sequence of the novelty where the polymorphic site within the sequence is  
 CC occupied by a base other than the reference base indicated in the  
 CC specification; and (3) analysing a nucleic acid, comprising obtaining a  
 CC nucleic acid from an individual, and determining a base occupying any one  
 CC of the polymorphic sites of the novelty. The nucleic acid segments and  
 CC method can be used to analyse an individual's nucleic acid sequences for  
 CC the presence of polymorphisms. The method can also be used to test for a  
 CC disease phenotype and correlate the presence of the phenotype with a  
 CC particular polymorphism. The presence of polymorphic sites are useful  
 CC for, e.g. forensics, paternity testing, correlation of polymorphisms  
 CC with phenotypic traits and for genetic mapping of phenotypic traits.  
 CC AAA/8631 to AAA/9262 represent sequence tags of human genomic DNA  
 CC fragments containing polymorphic sites. The base occupying the  
 CC polymorphic site is indicated using IUPAC-IUB nomenclature.  
 CC  
 SQ Sequence 31 BP; 4 A; 9 C; 11 G; 6 T; 1 other;  
 Query Match 0.6%; Score 30.6; DB 21; Length 31;  
 Best Local Similarity 96.8%; Pred. No. 9.1e+02;  
 Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4339 GGGACCCCACTGCTGCTGAGGGGCCCAT 4369  
 DB 1 GGGACCCCACTGCTGCTGAGGGGCCCAT 31  
 RESULT 11  
 AAA/9238  
 ID AAA/9238 standard; DNA; 31 BP.  
 XX  
 AC AAA/9238;  
 XX  
 DT 20-NOV-2000 (first entry)  
 XX  
 DE Human genomic DNA polymorphic site sequence tag SEQ ID NO:608.  
 XX  
 KW Human; genomic DNA; polymorphism; genome; allele-specific; primer;  
 KW probe; hybridisation; polymorphic site; forensic; paternity testing;  
 KW medicine; phenotypic trait; genetic analysis; genetic mapping; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EPI024200-A2.  
 XX  
 PD 02-AUG-2000.  
 XX

PE 26-JAN-2000; 2000EP-0250023.  
 XX 27-JAN-1999; 99US-0238402.  
 XX (AFFY-) AFFYMETRIX INC.  
 XX Patil N, Shah N, Warrington JA;  
 XX WPI; 2000-500198/45.  
 XX  
 XX Human genomic polymorphic nucleic acid segments, allele specific  
 PT primers and probes, and methods of analysis, useful for e.g. forensics,  
 PT paternity testing, genetic mapping,  
 XX  
 PS Claim 1; Page 22; 141pp; English.  
 CC The present invention describes a nucleic acid segment of 10-100  
 CC contiguous bases chosen from one of 632 fragments (AAA/8631 to  
 CC AAA/9262), where the segment comprises a polymorphic site or an  
 CC immediately adjacent base, or the complement of the segment. Also  
 CC described are: (1) an allele-specific oligonucleotide that hybridises to  
 CC a segment of the novelty; (2) an isolated nucleic acid comprising a  
 CC sequence of the novelty where the polymorphic site within the sequence is  
 CC occupied by a base other than the reference base indicated in the  
 CC specification; and (3) analysing a nucleic acid, comprising obtaining a  
 CC nucleic acid from an individual, and determining a base occupying any one  
 CC of the polymorphic sites of the novelty. The nucleic acid segments and  
 CC method can be used to analyse an individual's nucleic acid sequences for  
 CC the presence of polymorphisms. The method can also be used to test for a  
 CC disease phenotype and correlate the presence of the phenotype with a  
 CC particular polymorphism. The presence of polymorphic sites are useful  
 CC for, e.g. forensics, paternity testing, correlation of polymorphisms  
 CC with phenotypic traits and for genetic mapping of phenotypic traits.  
 CC AAA/8631 to AAA/9262 represent sequence tags of human genomic DNA  
 CC fragments containing polymorphic sites. The base occupying the  
 CC polymorphic site is indicated using IUPAC-IUB nomenclature.  
 CC  
 SQ Sequence 31 BP; 7 A; 7 C; 8 G; 8 T; 1 other;  
 Query Match 0.6%; Score 30.6; DB 21; Length 31;  
 Best Local Similarity 96.8%; Pred. No. 9.1e+02;  
 Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4449 GATCGAACACATCATGTGCGCAAGTCTGT 4479  
 DB 1 GATCGAACACATCATGTGCGCAAGTCTGT 31  
 RESULT 12  
 AAA/9239  
 ID AAA/9239 standard; DNA; 31 BP.  
 XX  
 AC AAA/9239;  
 XX  
 DT 20-NOV-2000 (first entry)  
 XX  
 DE Human genomic DNA polymorphic site sequence tag SEQ ID NO:609.  
 XX  
 KW Human; genomic DNA; polymorphism; genome; allele-specific; primer;  
 KW probe; hybridisation; polymorphic site; forensic; paternity testing;  
 KW medicine; phenotypic trait; genetic analysis; genetic mapping; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EPI024200-A2.  
 XX  
 PD 02-AUG-2000.  
 XX  
 PF 26-JAN-2000; 2000EP-0250023.  
 XX  
 PR 27-JAN-1999; 99US-0238402.  
 XX  
 PA (AFFY-) AFFYMETRIX INC.

```

XX  Patil N, Shah N, Warrington JA;
XX
DR  WPI; 2000-500198/45.
XX
XX  Human genomic polymorphic nucleic acid segments, allele specific
PT  primers and probes, and methods of analysis, useful for e.g. forensics,
PT  paternity testing, genetic mapping,
XX
XX  Claim 1; Page 22; 141pp; English.
XX
CC  The present invention describes a nucleic acid segment of 10-100
CC  contiguous bases chosen from one of 632 fragments (AA178631 to
CC  AA179267), where the segment comprises a polymorphic site or an
CC  immediately adjacent base, or the complement of the segment. Also
CC  described are: (1) an allele-specific oligonucleotide that hybridises to
CC  a segment of the novelty; (2) an isolated nucleic acid comprising a
CC  sequence of the novelty where the polymorphic site within the sequence is
CC  occupied by a base other than the reference base indicated in the
CC  specification; and (3) analysing a nucleic acid, comprising obtaining a
CC  nucleic acid from an individual, and determining a base occupying any one
CC  of the polymorphic sites of the novelty. The nucleic acid segments and
CC  method can be used to analyse an individual's nucleic acid sequences for
CC  the presence of polymorphisms. The method can also be used to test for a
CC  disease phenotype and correlate the presence of the phenotype with a
CC  particular polymorphism. The presence of polymorphic sites are useful
CC  for, e.g. forensics, paternity testing, correlation of polymorphisms
CC  with phenotypic traits and for genetic mapping of phenotypic traits.
CC  AA178631 to AA179267 represent sequence tags of human genomic DNA
CC  fragments containing polymorphic sites. The base occupying the
CC  polymorphic site is indicated using IUPAC-IUB nomenclature.
XX
XX  Sequence 31 BP; 5 A; 8 C; 9 G; 8 T; 1 other;
XX
XX  Query Match 0.6%; Score 30.6; DB 21; Length 31;
XX  Best Local Similarity 96.8%; Pred. No. 9.1e+02;
XX  Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0.
XX
QY  4722 GCCTTACCTAAAGTCCCGCGGTTCCGGCAT 4/52
DB  1 GCCTTACCTAAAGTCTCGCGGTTCCGGCAT 31
XX
RESULT 13
ID  AA033615/C
XX  AA033615 standard; DNA; 48 BP.
XX
AC  AA033615;
XX
XX  02-FEB-1993 (first entry)
XX
DE  Microsatellite sequence from clone AGLA33.
XX
XX  PCR: selection; primers: OPTIPRIM; breeding: cattle; parentage;
XX  genetic mapping; traits; amplification; ss.
XX
XX  Bos taurus.
XX
XX  MO9213102-A.
XX
XX  PD 06-AUG-1992.
XX
XX  15-JAN-1992; 92MO-US00340.
XX
XX  PE 15-JAN-1991; 91US-0642342.
XX
XX  (GENM-) GENMARK.
XX
XX  Georges M, Massey JM;
XX
XX  WPI; 1992-284684/34.
XX
XX  Polymorphic bovine DNA markers - used in genetic identification,
XX

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PT gene mapping, and selective breeding
XX
PS Table 7; Page 175-517pp; English.
CC
CX The sequence is that of a bovine microsatellite sequence obt. by
CC screening a library of bovine MboI DNA fragments of between
CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC One out of 50 clones cross-hybridised. Assuming independent
CC distribution of microsatellites and MboI sites, the frequency of
CC (T)n >9 microsatellites in the bovine genome is estimated at >100,
CC 000. The sequence information for ca. 230 such bovine microsatellites
CC is summarised in the specification and indexed herein (see below).
CC The sequences upstream and downstream of the microsatellite sequence
CC were used to generate the required PCR primers for in vitro
CC amplification of the corresp. microsatellite (using the program
CC OPTIPRM). The microsatellites may be used to identify individuals,
CC for percentage testing, and in the genetic mapping of economic trait
CC loci, or genes involved in the determinism of economically important
CC traits esp. in cattle, to allow selective breeding.
CC See also MAO33501-34437.
XX
XX Sequence 48 BP: 24 A; 0 C; 24 G; 0 U; 0 other;
PY
Q Query Match 0.5%; Score 28.4; DB 13; Length 48;
PY Best Local Similarity 76.1%; Pred.No.3.ee+03;
PY Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
PY
PY 264 CCCCCCCTCTCTCTTTCTCTCTCTCTCTCTCTGCTTGCTTCTGT 309
PY Db 48 CTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
PY
PY RESULT 14
PY AAS21107/C
PY ID AAS21107 standard; DNA; 50 BP.
PY XX
PY XX AAS21107:
PY DT 20-MAR-2002 (first entry)
PY XX
PY DE (GA)25 DNA purification oligonucleotide.
PY XX
PY KW ss; DNA purification; triple helix; plasmid purification.
PY OS Synthetic.
PY OS
PY FH Key Location/Qualifiers
PY FT repeat_region 1..50
PY FT /*tag= a
PY FT /*tag= b
PY FT /*tag= d
PY FT /note= "GA repeat type"
PY PN MO200192511-A2.
PY PD
PY PD 06-DEC-2001.
PY XX
PY PF 25-MAY-2001; 2001MO-US17122.
PY XX
PY PR 26-MAY-2000; 2000US-0580923.
PY XX
PY PA (AVET ) AVENTIS PHARMA SA.
PY XX
PY PI Crouzet J, Scherman D, Wils P, Blanche F, Cameron B;
PY DR WPI: 2002-097772/13.
PY PT Purifying double-stranded (ds) DNA from a solution containing dsDNA and
PY other components, comprises passing the solution through a support
PY comprising a covalently coupled oligonucleotide able to form a triple
PY helix with the dsDNA -
PY XX

```



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OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 20:53:31 ; Search time 161 seconds

(without alignments)  
9860.406 Million cell updates/sec

Title: US-10-003-919-3

Perfect score: 5273  
Sequence: 1 ctaggagcatgcacccacg.....aatctgccttcttaaaaa 5273

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA :  
1: /cgn2\_6/ptodata/1/lna/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/1/lna/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/lna/5A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/lna/5B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/lna/PCTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/lna/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	30.8	0.6	44	1 US-08-222-177A-385	Sequence 385, Appl
C 2	28.4	0.5	50	4 US-09-580-923-35	Sequence 35, Appl
C 3	28	0.5	47	3 US-08-933-358-18	Sequence 18, Appl
C 4	26.8	0.5	48	3 US-08-933-358-20	Sequence 20, Appl
C 5	25	0.5	47	4 US-09-641-638-934	Sequence 934, App
C 6	25	0.5	47	4 US-09-641-638-935	Sequence 935, App
C 7	24.8	0.5	28	4 US-09-281-481A-4	Sequence 4, Appl
C 8	24.4	0.5	28	4 US-09-281-481A-2	Sequence 2, Appl
C 9	23.6	0.4	32	1 US-08-469-802B-28	Sequence 28, Appl
C 10	23.6	0.4	32	2 US-08-267-803B-46	Sequence 46, Appl
C 11	23.4	0.4	34	1 US-08-418-123A-15	Sequence 15, Appl
C 12	23.4	0.4	35	1 US-08-418-123A-14	Sequence 14, Appl
C 13	23.4	0.4	36	1 US-08-418-123A-13	Sequence 13, Appl
C 14	23.4	0.4	37	1 US-08-418-123A-12	Sequence 12, Appl
C 15	23.4	0.4	38	1 US-08-418-123A-11	Sequence 11, Appl
C 16	23.4	0.4	39	1 US-08-418-123A-10	Sequence 10, Appl
C 17	23.4	0.4	40	1 US-08-418-123A-9	Sequence 9, Appl
C 18	23.4	0.4	41	1 US-08-418-123A-8	Sequence 8, Appl
C 19	23.4	0.4	42	1 US-08-418-123A-7	Sequence 7, Appl
C 20	23.4	0.4	43	1 US-08-418-123A-6	Sequence 6, Appl
C 21	23.4	0.4	44	1 US-08-418-123A-5	Sequence 5, Appl
C 22	23	0.4	45	2 US-08-495-695B-19	Sequence 19, Appl
C 23	23	0.4	45	5 PCT-US94-14435-19	Sequence 23, Appl
C 24	22.6	0.4	48	2 US-08-418-848A-23	Sequence 8, Appl
C 25	22.4	0.4	24	2 US-08-808-474A-8	Sequence 9, Appl
C 26	22.4	0.4	24	2 US-08-808-474A-9	Sequence 10, Appl
C 27	22.4	0.4	24	2 US-08-808-474A-10	Sequence 11, Appl

C 28	22.4	0.4	24	2 US-08-808-474A-11	Sequence 11, Appl
C 29	22.4	0.4	24	4 US-09-235-614-8	Sequence 8, Appl
C 30	22.4	0.4	24	4 US-09-235-614-9	Sequence 9, Appl
C 31	22.4	0.4	24	4 US-09-235-614-10	Sequence 10, Appl
C 32	22.4	0.4	24	4 US-09-235-614-11	Sequence 11, Appl
C 33	22.4	0.4	24	4 US-09-487-130-1	Sequence 1, Appl
C 34	22.4	0.4	24	4 US-09-487-130-2	Sequence 2, Appl
C 35	22.4	0.4	24	4 US-09-487-130-3	Sequence 3, Appl
C 36	22.4	0.4	24	4 US-09-487-130-4	Sequence 4, Appl
C 37	22.4	0.4	24	4 US-09-487-130-5	Sequence 5, Appl
C 38	22.4	0.4	24	4 US-09-487-130-6	Sequence 6, Appl
C 39	22.4	0.4	33	1 US-08-068-747-7	Sequence 7, Appl
C 40	22.4	0.4	33	1 US-08-418-123A-16	Sequence 16, Appl
C 41	22.4	0.4	43	1 US-08-418-123A-5	Sequence 5, Appl
C 42	22.4	0.4	50	3 US-08-846-020A-6	Sequence 6, Appl
C 43	22.4	0.4	50	4 US-09-617-871-6	Sequence 6, Appl
C 44	22.2	0.4	36	1 US-08-004-800-16	Sequence 16, Appl
C 45	22.2	0.4	36	1 US-08-413-813-16	Sequence 16, Appl

## ALIGNMENTS

RESULT 1  
US-08-222-177A-385/c  
Sequence 385, Application US/08222177A  
Patent No 5582979

GENERAL INFORMATION:

APPLICANT: Weber, James L.

TITLE OF INVENTION: LENGTH POLYMORPHISMS IN

NUMBER OF SEQUENCES: 460

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dewitt Ross & Stevens, S.C.

STREET: 8000 Excelsior Drive, Suite 401

CITY: Madison

STATE: Wisconsin

COUNTRY: USA

ZIP: 53717-1914

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/222,177A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/341,562

FILING DATE: 21-APR-1989

ATTORNEY/AGENT INFORMATION:

NAME: Sara, Charles S.

REGISTRATION NUMBER: 30,482

REFERENCE/DOCKET NUMBER: 09865.601

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 831-2100

TELEFAX: (608) 831-2106

TELEX:

INFORMATION FOR SEQ ID NO: 385:

SEQUENCE CHARACTERISTICS:

LENGTH: 44 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

MOLECULE TYPE: DNA (genomic)

IMMEDIATE SOURCE:

CLONE: mfd122rs

US-08-222-177A-385

Query Match

Best Local Similarity

Matches 35; Conservative

Score 30.8; DB 1; Length 44;

Pred. No. 65;

Mismatches 7; Indels 0; Gaps 0;







STREET: 300 S  
CITY: Chicago

Search completed: March 12, 2003, 02:53:00  
Job time : 171 secs

## RESULT 2

US-09-263-959-766  
; Sequence 766, Application US/09263959  
; Patent No. US20020150891A1  
; GENERAL INFORMATION:  
; APPLICANT: Hood, Leroy E.  
; APPLICANT: Rowen, Lee F.  
; APPLICANT: Koop, Ben F.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
; NUMBER OF SEQUENCES: 1279  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; City: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/263,959  
; FILING DATE: 05-MAR-1999  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMASTERS, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 920010.426C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 766:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 37 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-263-959-766  
Query Match 0.5%; Score 25.6; DB 10; Length 37;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 28; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 4408 ATATGATTAATTAATTAATTAATTAATTAAT 4439  
DB 2 ATAAATTAATTAATTAATTAATTAATTAAT 33  
RESULT 3  
US-09-735-363A-6  
; Sequence 6, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario  
; APPLICANT: Phillip, Nigel  
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
; FILE REFERENCE: 02811-0161  
; CURRENT APPLICATION NUMBER: US/09/735,363A  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; PRIOR APPLICATION NUMBER: 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: Patentin Version 3.0  
; SEQ ID NO 6  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-09-735-363A-6

Query Match 0.5%; Score 24.4; DB 10; Length 27;  
Best Local Similarity 96.2%; Pred. No. 2.5e+03;  
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 270 CTCCTCTCTCTCTCTCTCTCTCTCTCTCT 295  
DB 2 CTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 27  
RESULT 4  
US-09-263-959-474/c  
; Sequence 474, Application US/09263959  
; Patent No. US20020150891A1  
; GENERAL INFORMATION:  
; APPLICANT: Hood, Leroy E.  
; APPLICANT: Rowen, Lee F.  
; APPLICANT: Koop, Ben F.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH U  
; NUMBER OF SEQUENCES: 1279  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; City: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/263,959  
; FILING DATE: 05-MAR-1999  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMASTERS, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 920010.426C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 474:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-263-959-474  
Query Match 0.5%; Score 24.4; DB 10; Length 28;  
Best Local Similarity 96.2%; Pred. No. 2.6e+03;  
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 4414 ATAAATTAATTAATTAATTAATTAATTAAT 4439  
DB 28 ATAAATTAATTAATTAATTAATTAATTAAT 3  
RESULT 5  
US-09-740-002-4/c  
; Sequence 4, Application US/09740002  
; Patent No. US20020001798A1  
; GENERAL INFORMATION:  
; APPLICANT: BRAMS, PETER  
; APPLICANT: MORROW, PHILLIP  
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR  
; FILE REFERENCE: 037003-0275759  
; CURRENT APPLICATION NUMBER: US/09/740,002  
; CURRENT FILING DATE: 2000-12-20

Qy	271	TCCTCTCTTTCTCTCTCTCTCT	295
Db	26	TCCTCTCTCTCTCTCTCTCTCT	2

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OY      255 GGCACGGCCCCCCCCTCTCTCTTTCCTCTCT
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Db       35 GGASTGGRACGCCGTCTCTCTCTCTCTCTCTCT
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## RESULT 9

US-09-263-959-862/c  
; Sequence 862, Application US/09263959  
; Patent No. US20020150891A1  
; GENERAL INFORMATION:  
; APPLICANT: HOOD, LEROY E.  
; APPLICANT: Rowen, Ben F.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
; NUMBER OF SEQUENCES: 1279  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/09/263,959  
; FILING DATE: 05-MAR-1999  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mcmasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 920010.426C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 862:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-09-263-959-862

Query Match 0.4%; Score 22.4; DB 10; Length 24;  
Best Local Similarity 95.8%; Pred. No. 8.3e+03;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4416 AATAATATATATATATATATAT 4439  
|||||  
DB 24 AATAATATATATATATATATAT 1

RESULT 10  
US-09-988-899-55/c  
; Sequence 55, Application US/09988899  
; Patent No. US20020102613A1  
; GENERAL INFORMATION:  
; APPLICANT: HOOGERBOOM, HENDRICUS R.J.M.  
; TITLE OF INVENTION: NOVEL FAB FRAGMENT LIBRARIES AND METHOD FOR THEIR USE  
; FILE REFERENCE: DX/003 CON  
; CURRENT APPLICATION NUMBER: US/09/988,899  
; PRIOR FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: PCT/US00/13682  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: 99201558.6  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 55  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-988-899-55

Query Match 0.4%; Score 21.8; DB 10; Length 44;  
Best Local Similarity 67.4%; Pred. No. 1.8e+04;  
Matches 29; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

OY 2524 GTGACGAGTCCTCTGGAAGCTTATCCCTGTCACAGCTGT 2566  
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DB 43 GAGACTGCTGTCATGCTGAGTGTCAAGTGCACGTGTCGAGGCGGT 1

RESULT 11  
US-09-853-526-272  
; Sequence 272, Application US/09853526  
; Patent No. US20020165345A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Ilya, Chumakov  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: PROSTATE CANCER GENE  
; FILE REFERENCE: GENSET.1BCP1CP  
; CURRENT APPLICATION NUMBER: US/09/853,526  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: 09/738,907  
; PRIOR FILING DATE: 1999-06-23  
; PRIOR APPLICATION NUMBER: 08/996,306  
; PRIOR FILING DATE: 1997-12-22  
; PRIOR APPLICATION NUMBER: 60/099,658  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 09/218,207  
; PRIOR FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 578  
; SOFTWARE: Patent.pm  
; SEQ ID NO 272  
; LENGTH: 47  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 1..47  
; OTHER INFORMATION: polymorphic fragment 4-38-63, variant version of SRQ ID195  
; NAME/KEY: allele  
; LOCATION: 24  
; OTHER INFORMATION: base G; A in SRQ ID195  
; NAME/KEY: primer\_bind  
; LOCATION: 1..23  
; OTHER INFORMATION: potential microsequencing oligo 4-38-63.mls1  
; NAME/KEY: primer\_bind  
; LOCATION: 25..47  
; OTHER INFORMATION: complement potential microsequencing oligo 4-38-63.mls2  
US-09-853-526-272

Query Match 0.4%; Score 21.6; DB 9; Length 47;  
Best Local Similarity 75.0%; Pred. No. 2.2e+04;  
Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 2144 AAGTGAAGAAAGAACTGAGGCAACCAACTATAT 2179  
|||||  
DB 4 AAGTTATTAAGAAATCAAGGCGAGGCTAAACTTTT 39

RESULT 12  
US-09-901-484A-272  
; Sequence 272, Application US/09901484A  
; Patent No. US20020119460A1  
; GENERAL INFORMATION:  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: Prostate Cancer Gene  
; FILE REFERENCE: GEN-T11XC3D2  
; CURRENT APPLICATION NUMBER: US/09/901,484A  
; CURRENT FILING DATE: 2001-07-09

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; PRIOR APPLICATION NUMBER: US 08/996,306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: US 60/099,658
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: US 09/218,207
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/338,907
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: US 09/853,526
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 272
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1)..(47)
; OTHER INFORMATION: polymorphic fragment 4-38-63, variant version of SEQ ID 195
; NAME/KEY: allele
; LOCATION: (24)..(24)
; OTHER INFORMATION: polymorphic base G; A in SEQ ID 195
; NAME/KEY: primer_bind
; LOCATION: (1)..(23)
; OTHER INFORMATION: potential microsequencing oligo 4-38-63.m1s1
; NAME/KEY: primer_bind
; LOCATION: (25)..(47)
; OTHER INFORMATION: complement potential microsequencing oligo 4-38-63.m1s2
; US-09-901-484A-272

Query Match
Best Local Similarity 0.4%; Score 21.6; DB 10; Length 47;
Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 2144 AAGTGAAGAACTCAGCGCAACCAAACTATAT 2179
Db 4 AAGTATTAAGAAATCAGCGGAGGCTAACTTTT 39

RESULT 13
; Sequence 13, Application US/09845160
; Patent No. US20020058045A1
; GENERAL INFORMATION:
; APPLICANT: MIZUGUCHI, HIROYUKI
; TITLE OF INVENTION: ADENOVIRUS VECTOR
; FILE REFERENCE: 081356/0163
; CURRENT APPLICATION NUMBER: US/09/845,160
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: JP 2001-131688
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: JP 2000-161577
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 13
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Oligonucleotide 7.
; US-09-845-160-13

Query Match
Best Local Similarity 0.4%; Score 21.2; DB 10; Length 42;
Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 3922 CGCGCGCGCGCGCTGCTCAAGACCCGCGGCTGCTGC 3963
Db 1 CGCAGCGCGCGCGCTGCTCAAGACCCGCGGCTGCTGCACG 42
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; US-09-740-002-3/C
; Sequence 3, Application US/09740002
; Patent No. US20020001798A1
; GENERAL INFORMATION:
; APPLICANT: MORROW, PHILLIP
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
; FILE REFERENCE: 037003-0275759
; CURRENT APPLICATION NUMBER: US/09/740,002
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; US-09-740-002-3

Query Match
Best Local Similarity 0.4%; Score 21.2; DB 10; Length 47;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 258 CAGGCCCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 291
Db 34 CACTGACACCGCTCTCTCTCTCTCTCTCTCTCTCTCT 1

RESULT 15
; Sequence 44, Application US/10087523
; Publication No. US20020197624A1
; GENERAL INFORMATION:
; APPLICANT: Klein, Robert D.
; TITLE OF INVENTION: METHODS OF CREATING CONSTRUCTS USEFUL FOR INTRODUCING
; TITLE OF INVENTION: SEQUENCES INTO EMBRYONIC STEM CELLS
; FILE REFERENCE: 376472000200
; CURRENT APPLICATION NUMBER: US/10/087,523
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/193,834
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Plasmid vector
; US-10-087-523-44

Query Match
Best Local Similarity 0.4%; Score 21; DB 9; Length 50;
Matches 30; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 4323 CTCGCTCTGTACTGTGGACCCAGTGCCTGTTGAGCGCGCA 4367
Db 5 CTCGCTCTGTGTGCTGTGAATCCAGTGCAGATGTGTGGGACA 49

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Job time : 321 secs
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1  
2  
3  
4

5

6  
7

8  
9  
10  
11  
12

GenCore version 5.1.4-p5-4578  
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 20:47:25 ; Search time 6709 seconds  
(without alignments)  
12728.991 Million cell updates/sec

Title: US-10-003-919-3

Perfect score: 5273  
Sequence: 1 ctatggatgcatccacacg.....aatgtgccttcttaaaaa 5273

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: em\_estb:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estopl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gp\_est1:\*  
10: gp\_est2:\*  
11: gp\_hic:\*  
12: gp\_est3:\*  
13: gp\_est4:\*  
14: gp\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gp\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	0.6	49	10	AV674036
2	30	0.6	49	10	AV965544
3	29.8	0.6	41	17	AZ424284
4	29.6	0.6	40	17	AZ328467
5	29.4	0.6	47	10	AV949200
6	29.2	0.6	44	13	BJ001599

7	29.2	0.5	49	17	AZ846608
8	28.6	0.5	38	17	AZ79185
9	28.6	0.5	47	10	AV947640
10	28.4	0.5	38	17	AZ333216
11	28.4	0.5	47	17	AZ385990
12	28.4	0.5	47	17	AZ853064
13	28.4	0.5	47	17	AZ862836
14	28.4	0.5	47	17	AZ864870
15	28.4	0.5	49	9	AA773360
16	28.4	0.5	49	9	AA842027
17	28.4	0.5	49	9	A1813244
18	28.4	0.5	49	10	AV833587
19	28.4	0.5	49	13	BJ000259
20	28.4	0.5	50	17	AZ374770
21	28.2	0.5	42	10	AV957667
22	28.2	0.5	50	17	AZ655271
23	28	0.5	44	10	AV833550
24	28	0.5	47	17	AZ649857
25	27.8	0.5	50	17	AZ776590
26	27.6	0.5	40	10	AV833442
27	27.6	0.5	42	14	T54684
28	27.6	0.5	43	17	AZ345546
29	27.6	0.5	44	10	AV672475
30	27.6	0.5	47	17	AZ974579
31	27.6	0.5	47	17	AZ456727
32	27.6	0.5	50	14	BO577141
33	27.4	0.5	49	17	AZ790087
34	27.2	0.5	32	17	AZ329877
35	27.2	0.5	32	17	AZ515185
36	27.2	0.5	40	9	A1073810
37	27.2	0.5	41	10	AV672637
38	27.2	0.5	42	17	AZ826548
39	27.2	0.5	42	17	AZ941720
40	27.2	0.5	47	10	AV955412
41	27.2	0.5	50	12	BE976895
42	26.8	0.5	39	10	AV673727
43	26.8	0.5	49	10	AV671476
44	26.4	0.5	37	10	AV673465
45	26.4	0.5	37	17	AZ346663

## ALIGNMENTS

RESULT 1  
LOCUS AV674036 49 bp mRNA EST 05-OCT-2000  
DEFINITION AV674036 Mori Satoh unpublished cDNA library Clona Intestinalis  
ACCESSION AV674036  
VERSION AV674036.1 GI:10112035  
KEYWORDS  
SOURCE EST.  
ORGANISM Clona Intestinalis.  
Clona Intestinalis.  
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Clonidae; Clona.  
REFERENCE  
1 (bases 1 to 49)  
Satoh, N., Satoh, Y., Kohara, Y. and Shih, I.-T.  
Expressed genes in Clona Intestinalis  
Unpublished (2000)  
JOURNAL  
COMMENT Contact: Mori Satoh  
Department of zoology  
Kyoto University  
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: satoheacidian.zool.kyoto-u.ac.jp.

## FEATURES

1..49  
/organism="Clona Intestinalis"  
/db\_xref="taxon:7719"  
/clone="clb14a20"  
/clone\_lib="Mori Satoh unpublished cDNA library"









84112, USA  
Tel.: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
plate: 0114 row: D column: 16  
Seq primer: CACACAGCAACACGTATGACC  
Class: plasmid ends  
High quality sequence stop: 47.  
Location/Qualifiers  
1..47

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FEATURES
source
      84112, USA
      Tel: 801 585 5606
      Fax: 801 585 7177
      Email: ddunne@genetics.utah.edu
      Insert Length: 10000   Std Error: 0.00
      Plate: 0156   row: K   column: 04
      Seq primer: CCTGTAAACGACGCGCCACT
      Class: plasmid ends
      High quality sequence stop: 47.
      Location/Qualifiers
        1..47

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BASE COUNT
ORIGIN
0 a      23 c      0 g      24 t
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      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="DUGCJM0144D16"
      /clone.lib="Mouse 10kb plasmid DUGCJM library"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
      /note="Vector: pMD42nv; Purified genomic DNA from M.
      musculus C57BL/6J (male) was obtained from the Jackson
      Laboratory Mouse DNA Resource
      (http://www.jax.org/resources/documents/dnares/). The DNA
      was hydrodynamically sheared by repeated passage through a
      0.005 inch orifice at constant velocity. The sheared DNA
      was blunt end-repaired with T4 DNA polymerase and T4
      polynucleotide kinase. Adaptor oligonucleotides were
      ligated to the blunt ends in high molar excess. The
      digested DNA was purified and size-selected for a 9.5 to
      10.5 kb range using preparative agarose gel
      electrophoresis. Vector DNA was prepared from a derivative
      of pMD42 (g114732141g14732072.1), a copy-number
      inducible derivative of plasmid R1. The vector was ligated
      with adaptors complementary to the insert adaptors and
      purified. The sheared, adaptor mouse DNA was annealed to
      adaptor vector DNA, and transformed into
      chemically-competent E. coli XL10-Gold (Stratagene) cells
      and selected for ampicillin resistance."

```

BASE COUNT  
ORIGIN

0 a 23 c 0 g 24 t

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="tUGC2M0156K04"
/clone_lib="Mouse 10kb plasmid tUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, r1-resistant, F-"
/notes="Vector: pMD24nhv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD24 (g1147321141gb1AF129072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

	Query Match	0.5%	Score 28.4;	DB 17;	Length 47;
	Best Local Similarity	76.1%;	Pred. No.	3.1e+04;	
Matches	35; Conservative	0;	Mismatches	11; Indels	0;
GY	264 CCCCCCTCCTCTTTTCTCTCTCTCTGAGTGATTCGT	309			
Dd	2 CTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	47			

[illegible]

RESULT 12	
AZ853064	
LOCUS	47 bp DNA linear GSS 21-FEB-2001
DEFINITION	AZ853064 2M0156KR04F Mouse 10kb plasmid ucgcM1 library Mus musculus genomic
ACCESSION	clone ucgcM156KR04 F, DNA sequence.
VERSION	AZ853064
KEYWORDS	AZ853064.1 GI:13040804
SOURCE	GSS.
ORGANISM	house mouse.
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 47)
COMMENT	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
JOURNAL	Mouse whole genome scaffolding with paired end reads from 10kb
COMMENT	plasmid inserts
	Unpublished (2000)
	Contact: Robert B. Weiss
	University of Utah genome Center
	University of Utah
	Rm. 308, Biomedical polymers Research Bldg., 20 S. 2030 E., SLCC, UT

RESULT 13	
LOCUS	AZ862836
DEFINITION	47 bp DNA linear GSS 21-FEB-2001
ACCESSION	AZ862836
VERSION	2M0170N09 Mouse 10kb plasmid U0CUM library Mus musculus genomic
KEYWORDS	clone U0GC2M0170N09 R, DNA sequence.
SOURCE	AZ862836
ORGANISM	GSS.
REFERENCE	house mouse.
AUTHORS	Mus musculus.
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL	1 (passes 1 to 47)
COMMENT	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
	Mouse whole genome scaffolding with paired end reads from 10kb
	plasmid inserts
	Unpublished (2000)
	Contact: Robert B. Weiss
	University of Utah Genome Center
	Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112 USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert length: 10000 Std Error: 0.000  
Plates: 0174 Row: M Column: 10  
Seq primer: CACCACTGAACACACTTGTAC  
Class: plasmid ends  
high quality sequence, stop: 47.

/organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UDCC2M0174M10"  
 /clone\_id="Mouse 10kb plasmid UDCGIM library"  
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 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Cytogenetic DNA Resource  
 (<http://www.jax.org/resources/documents/dnares/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (911473211491AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

QY 264 CCCCCCTCTCTCTCTTTCTCTCTCTCTCTCTTGCCTTGCTTCCTGT 309

RESULT 15	LOCUS	DEFINITION	AA773360	49 bp	RNA	linear	EST 29-JAN-1998
	AA773360						
	IMAGE:845737	3' similar to gp.X63657-rnai					
		IMAGES:845737					
		3' similar to gp.X63657-rnai					
		FOLLICULAR VARIANT					

SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
human.	Homo sapiens	1 (bases 1 to 49)	Miller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kitzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steplewo, M., Tan, F., Thielking, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.	WashU-NCI human EST Project	unpublished (1997)	Contact: Wilson R

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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800

